P200301025DK SEQ listing.ST25
SEQUENCE LISTING

<110> Copenhagen University Tech Trans Enheden
Mundy, John

<120> Plant disease resistance and SAR regulator protein

<130> P200301025

<160> 28

<170> PatentIn version 3.2

<210> 1
<211> 669
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (1)..(669)

<400> 1

```
atg gat ccg tcg gag tat ttt gcc ggc ggc aat cct tcc gat caa cag      48
Met Asp Pro Ser Glu Tyr Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln
1               5                  10                  15

aac cag aag cgg cag ctt cag atc tgt ggt cct cgt cct tca cct ctt      96
Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
            20                  25                  30

agt gtt cac aaa gac tct cac aaa atc aag aaa cct cca aaa cac cct     144
Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
        35                  40                  45

gcg ccg ccg cca aat cgt gac caa ccg ccg ccg tat att cct aga gag     192
Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu
    50                  55                  60

ccg gtg gtt atc tac gcc gta tcc ccc aag gtt gta cac gca acc gcg     240
Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala
65                  70                  75                  80

tct gag ttc atg aac gta gtc cag cga ctc aca ggg atc tcc tct ggt     288
Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly
                85                  90                  95

gtt ttc ctc gaa tct ggc ggc ggt gga gat gtt tca ccg gcg gcg agg     336
Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg
            100                 105                 110

cta gcg tcc acg gaa aat gct agt cca aga gga gga aaa gaa ccg gct     384
Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala
        115                 120                 125

gcg aga gat gag acg gtg gaa atc aac acg gct atg gaa gaa gca gct     432
Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala
    130                 135                 140

gaa ttt ggt ggt tat gct ccg gga ata ctc tcg cca tct ccg gcc ttg     480
Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu
145                 150                 155                 160

ttg cca aca gct tct acc ggg ata ttc tct ccg atg tat cat caa ggt     528
Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly
                165                 170                 175
```

ggg atg ttt tcg ccg gct ata cca ctg gga tta ttc tcg ccg gcg gga 576
Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly
180 185 190

ttt atg agc ccg ttt cga agt cct ggc ttt act agt ttg gta gct tca 624
Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser
195 200 205

cca act ttt gct gat ttc ttt agt cat att tgg gat caa gat tag 669
Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp
210 215 220

<210> 2
<211> 222
<212> PRT
<213> Arabidopsis sp.

<400> 2

Met Asp Pro Ser Glu Tyr Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln
1 5 10 15

Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
20 25 30

Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
35 40 45

Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu
50 55 60

Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala
65 70 75 80

Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly
85 90 95

Val Phe Leu Glu Ser Gly Gly Gly Gly Asp Val Ser Pro Ala Ala Arg
100 105 110

Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala
115 120 125

Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala
130 135 140

Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu
145 150 155 160

Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly
165 170 175

Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly
180 185 190

Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser
195 200 205

Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp
210 215 220

<210> 3
<211> 16
<212> DNA
<213> Arabidopsis sp.

<400> 3
atggatccgt cggagt 16

<210> 4
<211> 16
<212> DNA
<213> Arabidopsis sp.

<400> 4
ctaatcttca tcccaa 16

<210> 5
<211> 720
<212> DNA
<213> Arabidopsis sp.

<220>
<221> CDS
<222> (1)..(720)

<400> 5
atg gat aat aga tcg cca aga tca aga gga atc ttg ggt ccg aga cca 48
Met Asp Asn Arg Ser Pro Arg Ser Arg Gly Ile Leu Gly Pro Arg Pro
1 5 10 15

ata cca ttg aaa gtc cgt gga gat tcg cac aag atc atc aag aag cca 96
Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro
20 25 30

cca cta gcg ccg cca cac ccg caa cca caa cca cca caa acc cat cag 144
Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln
35 40 45

caa gaa ccg tca caa tcg cgg ccg cca cct ggt ccc gtg att ata tac 192
Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr
50 55 60

aca gta tct ccc agg att atc cat aca cac cct aat aac ttc atg aca 240
Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr
65 70 75 80

ttg gtc caa cgt ctc aca ggt aaa acc tcc acc tcc aca aca tcc tcc 288
Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser
85 90 95

tcc tat tct tca tct acg tca gca cca aaa gac gcg tca aca atg gtt 336
Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val
100 105 110

gat aca tct cat ggg ttg ata tct ccg gcg gct cgg ttt gct gtt aca 384
Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
115 120 125

```
gag aag gct aat atc tca aac gaa cta ggg aca ttt gtt gga ggc gaa      432
Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu
    130                 135                 140

ggg act atg gat caa tat tat cat tat cat cat cat cat cat cat caa      480
Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His His Gln
145                 150                 155                 160

gaa caa caa cat caa aat caa ggg ttc gag cgg cca agt ttc cac cat      528
Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His
                165                 170                 175

gct ggg att tta tcg ccg gga cct aat tct ctg ccg tcg gta tca ccg      576
Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro
            180                 185                 190

gac ttc ttt tcc act att gga cca acc gat cca caa ggt ttt tcg tcg      624
Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser
        195                 200                 205

ttc ttt aat gac ttt aac tct atc ctt cag agt agt cca tcg aag att      672
Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile
    210                 215                 220

cag tct cct tct tct atg gac ctt ttc aac aat ttc ttt gat tct tga      720
Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser
225                 230                 235
```

<210> 6
<211> 239
<212> PRT
<213> Arabidopsis sp.

<400> 6

```
Met Asp Asn Arg Ser Pro Arg Ser Arg Gly Ile Leu Gly Pro Arg Pro
1               5                   10                  15

Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro
            20                  25                  30

Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln
        35                  40                  45

Gln Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr
    50                  55                  60

Thr Val Ser Pro Arg Ile Ile His Thr His Pro Asn Asn Phe Met Thr
65                  70                  75                  80

Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser
                85                  90                  95

Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val
            100                 105                 110

Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
        115                 120                 125
```

Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Gly Glu
130 135 140

Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His His Gln
145 150 155 160

Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His
165 170 175

Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro
180 185 190

Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser
195 200 205

Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile
210 215 220

Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser
225 230 235

<210> 7
<211> 20
<212> DNA
<213> Arabidopsis sp.

<400> 7
atggataata gatcgccaag 20

<210> 8
<211> 21
<212> DNA
<213> Arabidopsis sp.

<400> 8
tcaagaatca aagaaattgt t 21

<210> 9
<211> 791
<212> DNA
<213> Brassica oleracea

<220>
<221> CDS
<222> (139)..(789)

<400> 9
taatttttcc ctttttttt tgtttataaa tgttttggtc aatactagct cgtcgtcgac 60

aaagattcat ttcgattccc aaaccacaca agaagaacac aaattagctc gaaagaaaca 120

aactcttttg agaaaata atg gat ccg tcg gag tct ttc gcc ggc ggc aat 171
Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn
1 5 10

cct tcc gac caa cag aac cag aaa cgt cag ctt cag atc tgt ggt cct 219
Pro Ser Asp Gln Gln Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro

15 20 25

cgt ccc tca cct ctc agc gtc aac aaa gac tct cac aag atc aag aaa 267
Arg Pro Ser Pro Leu Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys
30 35 40

cct cct aaa cac cct gct cct ccg cct cag cat cgc gac caa gct ccg 315
Pro Pro Lys His Pro Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro
45 50 55

ctc tac gct gct cga gag ccg gtg gtc atc tac gcc gtc tcg ccg aaa 363
Leu Tyr Ala Ala Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys
60 65 70 75

gtc gtc cac acc aca gcc tcg gat ttc atg aac gtc gtc cag cgt ctc 411
Val Val His Thr Thr Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu
80 85 90

acc ggc atc tca tcc gcc gtc ttc ctc gaa tcc ggt aac ggc gga gat 459
Thr Gly Ile Ser Ser Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp
95 100 105

gta tct ccg gcg gcg aga ctc gcc gcg acc gag aat gca agc ccg aga 507
Val Ser Pro Ala Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg
110 115 120

gga gga aaa gaa ccg gtg atg gcg gct aaa gat gag acg gtg gaa atc 555
Gly Gly Lys Glu Pro Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile
125 130 135

gcg acg gct atg gaa gaa gca gcc gag ttg agc ggc tat gcg ccg ggg 603
Ala Thr Ala Met Glu Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly
140 145 150 155

ata ctc tcc cct tct ccg gct atg tta ccg aca gct tct gcc gga ata 651
Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile
160 165 170

ttc tcg cag atg act act cac caa ggt ggg atg ttc tcg ccg gga ttg 699
Phe Ser Gln Met Thr Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu
175 180 185

ttt tcg ccg gcg ggg tta atg agc ccg ttt ggt ttt gct agc ttg gtt 747
Phe Ser Pro Ala Gly Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val
190 195 200

gct tct cca acg ttt gct gat ttg ttc agt cat att tgg gga ta 791
Ala Ser Pro Thr Phe Ala Asp Leu Phe Ser His Ile Trp Gly
205 210 215

<210> 10
<211> 217
<212> PRT
<213> Brassica oleracea

<400> 10

Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln
1 5 10 15

Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
20 25 30

Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
35 40 45

Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg
50 55 60

Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr
65 70 75 80

Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser
85 90 95

Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp Val Ser Pro Ala Ala
100 105 110

Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro
115 120 125

Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu
130 135 140

Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser
145 150 155 160

Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr
165 170 175

Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly
180 185 190

Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val Ala Ser Pro Thr Phe
195 200 205

Ala Asp Leu Phe Ser His Ile Trp Gly
210 215

<210> 11
<211> 20
<212> DNA
<213> Brassica oleracea

<400> 11
atggatccgt cggagtcttt 20

<210> 12
<211> 20
<212> DNA
<213> Brassica oleracea

<400> 12
tatccccaaa tatgactgaa 20

<210> 13
<211> 878
<212> DNA
<213> Brassica oleracea

<220>
<221> CDS
<222> (198)..(833)

<400> 13
aaaagtcaac attttgaaag tcaaactaat cggtctcaga aaacaaaaat aactttgtgt 60

gttgatgttt aggtcaatat actcgtcgtc aaaacatccc ttcaatttct cagaccaaac 120

acagagaaga aacaagttgg atccaaactc tctacaacaa aaagtagtga acgagagaag 180

ctctccccaa gcgttta atg gat ccg tcg gag cac ttc gcc ggc ggt aat 230
Met Asp Pro Ser Glu His Phe Ala Gly Gly Asn
1 5 10

cct ttc gat caa cag act cca aaa cgt cag ctt cag atc tgt ggc cct 278
Pro Phe Asp Gln Gln Thr Pro Lys Arg Gln Leu Gln Ile Cys Gly Pro
15 20 25

cgt cct tca cct cta agc gtc aac aaa gac tct cac aag atc aag aaa 326
Arg Pro Ser Pro Leu Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys
30 35 40

cct ccc agg cac cct gct cca cct cct cag cat cac cgc gac caa gct 374
Pro Pro Arg His Pro Ala Pro Pro Pro Gln His His Arg Asp Gln Ala
45 50 55

ccg ctc tac cct cct cga gag ccg gtg gtt atc tac gcc gtc tcg ccg 422
Pro Leu Tyr Pro Pro Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro
60 65 70 75

aaa gtc gtg cac acc aca acc tcc gat ttc atg aac gtc gtc cag cgt 470
Lys Val Val His Thr Thr Thr Ser Asp Phe Met Asn Val Val Gln Arg
80 85 90

ctc acc ggg atc tcc tcc gag gtc ttc ctc gaa tca aga aac gac gga 518
Leu Thr Gly Ile Ser Ser Glu Val Phe Leu Glu Ser Arg Asn Asp Gly
95 100 105

gat gta tca ccg gcg gcg aga ctc gcc gcg acg gag aat gct agc ccg 566
Asp Val Ser Pro Ala Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro
110 115 120

aga gga gga aag gaa ccg gtg gaa agc tcg acg gct atg gaa gaa gca 614
Arg Gly Gly Lys Glu Pro Val Glu Ser Ser Thr Ala Met Glu Glu Ala
125 130 135

gct gag ttc ggt tgt tat gtg ccg gga ata ctc tcg ccg tct ccg gct 662
Ala Glu Phe Gly Cys Tyr Val Pro Gly Ile Leu Ser Pro Ser Pro Ala
140 145 150 155

atg tta ccg acc gtt ccc gcc gga att ttc tct ccg atg ttt cac cta 710
Met Leu Pro Thr Val Pro Ala Gly Ile Phe Ser Pro Met Phe His Leu
160 165 170

ggt ggg ttg ttt tcg ccg gcg ttg ccg ccg gga tta ttt tcg ccg gca 758
Gly Gly Leu Phe Ser Pro Ala Leu Pro Pro Gly Leu Phe Ser Pro Ala
175 180 185

gga tta atg agc cct ggt tat gct agt ttg gcg tca cca aat ttt gct 806
Gly Leu Met Ser Pro Gly Tyr Ala Ser Leu Ala Ser Pro Asn Phe Ala
190 195 200

gat ttc ttc agt cac att tgg gat cct tagagaatag attattagtt 853
Asp Phe Phe Ser His Ile Trp Asp Pro
205 210

tttttttatta tttacatttt atgta 878

<210> 14
<211> 212
<212> PRT
<213> Brassica oleracea

<400> 14

Met Asp Pro Ser Glu His Phe Ala Gly Gly Asn Pro Phe Asp Gln Gln
1 5 10 15

Thr Pro Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
20 25 30

Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Arg His Pro
35 40 45

Ala Pro Pro Pro Gln His His Arg Asp Gln Ala Pro Leu Tyr Pro Pro
50 55 60

Arg Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr
65 70 75 80

Thr Thr Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser
85 90 95

Ser Glu Val Phe Leu Glu Ser Arg Asn Asp Gly Asp Val Ser Pro Ala
100 105 110

Ala Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu
115 120 125

Pro Val Glu Ser Ser Thr Ala Met Glu Glu Ala Ala Glu Phe Gly Cys
130 135 140

Tyr Val Pro Gly Ile Leu Ser Pro Ser Pro Ala Met Leu Pro Thr Val
145 150 155 160

Pro Ala Gly Ile Phe Ser Pro Met Phe His Leu Gly Gly Leu Phe Ser
165 170 175

Pro Ala Leu Pro Pro Gly Leu Phe Ser Pro Ala Gly Leu Met Ser Pro
180 185 190

Gly Tyr Ala Ser Leu Ala Ser Pro Asn Phe Ala Asp Phe Phe Ser His
195 200 205

Ile Trp Asp Pro
210

<210> 15

P200301025DK SEQ listing.ST25

<211> 393
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(393)

<400> 15

```
caa ctt caa ggt cca cgc cct aca cct ctc aga ata aac aaa gac tct       48
Gln Leu Gln Gly Pro Arg Pro Thr Pro Leu Arg Ile Asn Lys Asp Ser
1               5                   10                  15

cat aaa atc aag aaa cca ccg ttg gca cca caa cct tca cac cct cat       96
His Lys Ile Lys Lys Pro Pro Leu Ala Pro Gln Pro Ser His Pro His
            20                  25                  30

caa cct cca ccg cgc caa cct ata ata atc tac acc gtg tcc ccc aag      144
Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys
        35                  40                  45

gtg att cac acc acc cca agt gac ttc atg aac ctc gtc caa cgc ctc      192
Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu
    50                  55                  60

act ggg tcc agt tct tct tcc tct gct gaa gtg gtc atg tcc aac aat      240
Thr Gly Ser Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn
65                  70                  75                  80

aac aac acc act cat gtc gac cct ttc aac aac ggc ggc ggc gga atg      288
Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Gly Met
                85                  90                  95

gtg tcg ccg gcg gcg cgt tac gcc acc ata gag aag gcc atg tcc cct      336
Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro
            100                 105                 110

atg ggg aaa aaa cat gtt ctt ctt cca agt gtg aac aat att ata agc      384
Met Gly Lys Lys His Val Leu Leu Pro Ser Val Asn Asn Ile Ile Ser
        115                 120                 125

gat gtg gaa                                                         393
Asp Val Glu
    130
```

<210> 16
<211> 131
<212> PRT
<213> Glycine max

<400> 16

```
Gln Leu Gln Gly Pro Arg Pro Thr Pro Leu Arg Ile Asn Lys Asp Ser
1               5                   10                  15

His Lys Ile Lys Lys Pro Pro Leu Ala Pro Gln Pro Ser His Pro His
            20                  25                  30

Gln Pro Pro Pro Arg Gln Pro Ile Ile Ile Tyr Thr Val Ser Pro Lys
        35                  40                  45

Val Ile His Thr Thr Pro Ser Asp Phe Met Asn Leu Val Gln Arg Leu
    50                  55                  60
```

Thr Gly Ser Ser Ser Ser Ser Ser Ala Glu Val Val Met Ser Asn Asn
65 70 75 80

Asn Asn Thr Thr His Val Asp Pro Phe Asn Asn Gly Gly Gly Gly Met
85 90 95

Val Ser Pro Ala Ala Arg Tyr Ala Thr Ile Glu Lys Ala Met Ser Pro
100 105 110

Met Gly Lys Lys His Val Leu Leu Pro Ser Val Asn Asn Ile Ile Ser
115 120 125

Asp Val Glu
130

<210> 17
<211> 19
<212> DNA
<213> Glycine max

<400> 17
ccatagagaa ggccatgtc 19

<210> 18
<211> 20
<212> DNA
<213> Glycine max

<400> 18
tgaatgttgt ggtgccaacg 20

<210> 19
<211> 927
<212> DNA
<213> Oryza sp.

<220>
<221> CDS
<222> (7)..(927)

<400> 19
gtggcg atg gaa ttc ccg tcg tcg acg tcg ccg tcg ccg tcg ccg tcg 48
Met Glu Phe Pro Ser Ser Thr Ser Pro Ser Pro Ser Pro Ser
1 5 10

tcc ggg cag cat cag cag cag ccg acg acg ccg cgg cgg cag ctt cag 96
Ser Gly Gln His Gln Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln
15 20 25 30

ggc ccg cgc ccc ccg cgg ctc aac gtg cgg atg gag tcg cac gcc atc 144
Gly Pro Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His Ala Ile
35 40 45

aag aag ccg tcg tcc ggg gcg gcc gcg gcg gcg gcg gcg gcg cag gcg 192
Lys Lys Pro Ser Ser Gly Ala Ala Ala Ala Ala Ala Ala Gln Ala
50 55 60

agg cgg gag cag cag cag ccg ccg ccg cgg gcg ccg gtg atc atc tac 240

P200301025DK SEQ listing.ST25

```
Arg Arg Glu Gln Gln Gln Pro Pro Pro Arg Ala Pro Val Ile Ile Tyr
        65                  70                  75

gac gcg tcg ccg aag att atc cac gcc aag ccc aac gag ttc atg gcg      288
Asp Ala Ser Pro Lys Ile Ile His Ala Lys Pro Asn Glu Phe Met Ala
    80                  85                  90

ctc gtg cag cgg ctc acc ggc ccg ggg tcg ggg ccg ccg gcg ccg ccg      336
Leu Val Gln Arg Leu Thr Gly Pro Gly Ser Gly Pro Pro Ala Pro Pro
95                  100                 105                 110

cat caa ggg gag gcc cag gcg cag gac tac ccg atg atg gac gag gcc      384
His Gln Gly Glu Ala Gln Ala Gln Asp Tyr Pro Met Met Asp Glu Ala
                115                 120                 125

gcc gcg cag cag ttc ttc ccg ccg gag ctg ctg ctc tcg ccg tcg gcc      432
Ala Ala Gln Gln Phe Phe Pro Pro Glu Leu Leu Leu Ser Pro Ser Ala
            130                 135                 140

gcg atg tcc ccg gcg gcg agg ctg gcg acc atc gag agg tcc gtc cgc      480
Ala Met Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg Ser Val Arg
        145                 150                 155

ccg atg ccc gag ccg gcg ccg gag tac gtg gac atc acg aac ggc ggc      528
Pro Met Pro Glu Pro Ala Pro Glu Tyr Val Asp Ile Thr Asn Gly Gly
    160                 165                 170

ggc ggc ggc ggg gtc gac gac ggc ggc ctc gcg gcg atc ctc ggc tcg      576
Gly Gly Gly Gly Val Asp Asp Gly Gly Leu Ala Ala Ile Leu Gly Ser
175                 180                 185                 190

atc cgg cca ggc atc ctc tcc ccg ctc ccc tcc tcc ctc ccg ccc gcc      624
Ile Arg Pro Gly Ile Leu Ser Pro Leu Pro Ser Ser Leu Pro Pro Ala
                195                 200                 205

gcc gtc ccc ggc cag ttc tcg ccg ctc ccg ttc gac gcg agg ccg ctc      672
Ala Val Pro Gly Gln Phe Ser Pro Leu Pro Phe Asp Ala Arg Pro Leu
            210                 215                 220

ccg ttc gac gcg agc tgc atc agc tgg ctc aac gag ctg agc ccc atc      720
Pro Phe Asp Ala Ser Cys Ile Ser Trp Leu Asn Glu Leu Ser Pro Ile
        225                 230                 235

ctc cgg gcc gcc tcc gcc ggc gcg gcc tcg tcc ggc agc ggc ggc ggc      768
Leu Arg Ala Ala Ser Ala Gly Ala Ala Ser Ser Gly Ser Gly Gly Gly
    240                 245                 250

ggc agc ggt ggc aac acc agc aac ggc ggc ggc gcc cgc ccg ccg ccg      816
Gly Ser Gly Gly Asn Thr Ser Asn Gly Gly Gly Ala Arg Pro Pro Pro
255                 260                 265                 270

tcc tac tac gcc gac cca ttc gtc ccc agc cca cgt cac ctc ctc gcc      864
Ser Tyr Tyr Ala Asp Pro Phe Val Pro Ser Pro Arg His Leu Leu Ala
                275                 280                 285

acg ccc acc gtg ccg tcg ccg gcg acc tgc gcc gag ctc ttc agc aac      912
Thr Pro Thr Val Pro Ser Pro Ala Thr Cys Ala Glu Leu Phe Ser Asn
            290                 295                 300

ctg ccg gat ctc tag                                                  927
Leu Pro Asp Leu
        305
```

<210> 20
<211> 306
<212> PRT
<213> Oryza sp.

P200301025DK SEQ listing.ST25

<400> 20

Met Glu Phe Pro Ser Ser Thr Ser Pro Ser Pro Ser Pro Ser Ser Gly
1 5 10 15

Gln His Gln Gln Gln Pro Thr Thr Pro Arg Arg Gln Leu Gln Gly Pro
20 25 30

Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His Ala Ile Lys Lys
35 40 45

Pro Ser Ser Gly Ala Ala Ala Ala Ala Ala Ala Ala Gln Ala Arg Arg
50 55 60

Glu Gln Gln Gln Pro Pro Pro Arg Ala Pro Val Ile Ile Tyr Asp Ala
65 70 75 80

Ser Pro Lys Ile Ile His Ala Lys Pro Asn Glu Phe Met Ala Leu Val
85 90 95

Gln Arg Leu Thr Gly Pro Gly Ser Gly Pro Pro Ala Pro Pro His Gln
100 105 110

Gly Glu Ala Gln Ala Gln Asp Tyr Pro Met Met Asp Glu Ala Ala Ala
115 120 125

Gln Gln Phe Phe Pro Pro Glu Leu Leu Leu Ser Pro Ser Ala Ala Met
130 135 140

Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg Ser Val Arg Pro Met
145 150 155 160

Pro Glu Pro Ala Pro Glu Tyr Val Asp Ile Thr Asn Gly Gly Gly Gly
165 170 175

Gly Gly Val Asp Asp Gly Gly Leu Ala Ala Ile Leu Gly Ser Ile Arg
180 185 190

Pro Gly Ile Leu Ser Pro Leu Pro Ser Ser Leu Pro Pro Ala Ala Val
195 200 205

Pro Gly Gln Phe Ser Pro Leu Pro Phe Asp Ala Arg Pro Leu Pro Phe
210 215 220

Asp Ala Ser Cys Ile Ser Trp Leu Asn Glu Leu Ser Pro Ile Leu Arg
225 230 235 240

Ala Ala Ser Ala Gly Ala Ala Ser Ser Gly Ser Gly Gly Gly Gly Ser
245 250 255

Gly Gly Asn Thr Ser Asn Gly Gly Gly Ala Arg Pro Pro Pro Ser Tyr

260 265 270

Tyr Ala Asp Pro Phe Val Pro Ser Pro Arg His Leu Leu Ala Thr Pro
275 280 285

Thr Val Pro Ser Pro Ala Thr Cys Ala Glu Leu Phe Ser Asn Leu Pro
290 295 300

Asp Leu
305

<210> 21
<211> 16
<212> DNA
<213> Oryza sp.

<400> 21
atggaattcc cgtcgt 16

<210> 22
<211> 19
<212> DNA
<213> Oryza sp.

<400> 22
ctagagatcc ggcaggttg 19

<210> 23
<211> 781
<212> DNA
<213> CaMV 35S promoter duplicated

<400> 23
atggtggagc acgacactct cgtctactcc aagaatatca aagatacagt ctcagaagac 60
caaagggcta ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat 120
tgcccagcta tctgtcactt catcaaaagg acagtagaaa aggaaggtgg cacctacaaa 180
tgccatcatt gcgataaagg aaaggctatc gttcaagatg cctctgccga cagtggtccc 240
aaagatggac ccccacccac gaggagcatc gtggaaaaag aagacgttcc aaccacgtct 300
tcaaagcaag tggattgatg tgataacatg gtggagcacg acactctcgt ctactccaag 360
aatatcaaag atacagtctc agaagaccaa agggctattg agacttttca acaaagggta 420
atatcgggaa acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca 480
gtagaaaagg aaggtggcac ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt 540
caagatgcct ctgccgacag tggtcccaaa gatggacccc cacccacgag gagcatcgtg 600
gaaaaagaag acgttccaac cacgtcttca aagcaagtgg attgatgtga tatctccact 660
gacgtaaggg atgacgcaca atcccactat ccttcgcaag accttcctct atataaggaa 720
gttcatttca tttggagagg acacgctgaa atcaccagtc tctctctaca aatctatctc 780
t 781

P200301025DK SEQ listing.ST25

<210> 24
<211> 253
<212> DNA
<213> Agrobacterium NOS terminator

<400> 24
cgttcaaaca tttggcaata aagtttctta agattgaatc ctgttgccgg tcttgcgatg 60

attatcatat aatttctgtt gaattacgtt aagcatgtaa taattaacat gtaatgcatg 120

acgttattta tgagatgggt ttttatgatt agagtcccgc aattatacat ttaatacgcg 180

atagaaaaca aaatatagcg cgcaaactag gataaattat cgcgcgcggt gtcatctatg 240

ttactagatc ggg 253

<210> 25
<211> 189
<212> DNA
<213> Synthetic intron

<400> 25
gtaagtttct gcttctacct ttgatatata taataataat atcattaatt agtagtaata 60

taatatttca aatatttttt tcaaaataaa agaatgtagt atatagcaat tgcttttctg 120

tagtttataa gtgtgtatat tttaatttat aacttttcta atatatgacc aaaatttgtt 180

gatgtgcag 189

<210> 26
<211> 207
<212> PRT
<213> Oryza sp.

<400> 26

Met Glu Gln Gln Leu Ser Ser Pro Ser Ala Ser Gln Arg Gly Gly Gly
1 5 10 15

Arg Glu Leu Gln Gly Pro Arg Pro Ala Pro Leu Lys Val Arg Lys Glu
20 25 30

Ser His Lys Ile Arg Lys Gln Glu Pro Val Gln Gln Leu Arg Gln Pro
35 40 45

Val Ile Ile Tyr Thr Met Ser Pro Lys Val Val His Ala Asn Ala Ala
50 55 60

Asp Phe Met Ser Val Val Gln Arg Leu Thr Gly Ala Pro Pro Thr Ala
65 70 75 80

Pro Pro Gln Pro Gln Pro His His Pro Thr Leu Leu Ala Gln Met Pro
85 90 95

Pro Gln Pro Ser Phe Pro Phe His Leu Gln Gln Gln Asp Ala Trp Pro
100 105 110

Gln Gln Gln His Ser Pro Ala Ala Ile Glu Gln Ala Ala Ala Arg Ser

115 120 125

Ser Gly Ala Asp Leu Pro Pro Leu Pro Ser Ile Leu Ser Pro Val Pro
130 135 140

Gly Thr Val Leu Pro Ala Ile Pro Ala Ser Phe Phe Ser Pro Pro Ser
145 150 155 160

Leu Ile Ser Pro Val Pro Phe Leu Gly Ala Thr Thr Thr Ser Ser Ala
165 170 175

Ala Pro Ser Thr Ser Pro Ser Pro Met Gly Gly Ser Ala Tyr Tyr Trp
180 185 190

Asp Leu Phe Asn Met Gln Gln Gln Gln His Tyr His His Gln Asn
195 200 205

<210> 27
<211> 238
<212> PRT
<213> Zea mays

<400> 27

Met Asp Pro Pro Ser Ser Ser Gly Arg Pro Thr Thr Pro Arg Arg Gln
1 5 10 15

Leu Gln Gly Pro Arg Pro Pro Arg Leu Asn Val Arg Met Glu Ser His
20 25 30

Ala Ile Lys Lys Pro Ser Ala Ser Gly Ala Pro Pro Ala Pro Gly Gln
35 40 45

Gly Arg Pro Arg Asp His His His His His Pro Gln Pro Gly Arg Ala
50 55 60

Pro Val Ile Ile Tyr Asp Ala Ser Pro Lys Val Ile His Ala Lys Pro
65 70 75 80

Ser Glu Phe Met Ala Leu Val Gln Arg Leu Thr Gly Pro Gly Ala Gln
85 90 95

Ala Gln His Glu Arg His Val Ala Asp Asp Asp Ala Thr Ala Asn Gly
100 105 110

Gly Gly Val Leu Gly Gln Ala Phe Leu Pro Pro Glu Leu Leu Leu Ser
115 120 125

Pro Ser Ala Ala Met Ser Pro Ala Ala Arg Leu Ala Thr Ile Glu Arg
130 135 140

Ser Val Arg Pro Val Pro Ala Pro Ala Pro Ala Pro Asp Tyr Ala Ala
145 150 155 160

Asp Gly His Pro Arg Gly Gly Ala Arg Pro Arg Glu Ala Pro Arg His
165 170 175

Pro Val Pro Ala Ala Val Leu Ala Ala Ala Gly Arg Arg Val Gly Pro
180 185 190

Val Leu Ala Ala Ala Leu Arg Pro Gln Gln Arg Gln Leu Ala Gln Arg
195 200 205

Ala Gln Pro His Pro Pro Gly Ser Val His Gly Gln Arg Ser Ala Pro
210 215 220

Leu Ala His Ala His Gly Pro Thr Gly Gly Ser Arg Gln Pro
225 230 235

<210> 28
<211> 271
<212> PRT
<213> Zea mays

<400> 28

Gln Gly Pro Arg Pro Pro Arg Leu Ala Val Ser Lys Asp Ser His Lys
1 5 10 15

Val Arg Lys Pro Pro Val Ala Pro Gln Arg Gln Gln His Gln His Gln
20 25 30

Gln Pro Ala Ala Gln Leu Gln Gln Gln Gln His Gln Tyr His Gln Gln
35 40 45

Gln Gln Gln Gln Gly Arg Gln Pro Val Ile Ile Tyr Asp Ala Ser Pro
50 55 60

Lys Val Ile His Thr Lys Pro Gly Asp Phe Met Ala Leu Val Gln Arg
65 70 75 80

Leu Thr Gly Pro Gly Ser Thr Ser Gln Ala Gln Phe Asp Ala Ala Ala
85 90 95

Ala Ala Ala Gly Pro Ser His Pro Ala Ala Met Glu Phe Glu Pro Arg
100 105 110

Glu Phe Leu Leu Ser Pro Thr Ala Ala Leu Ser Pro Ala Ala Arg Leu
115 120 125

Ala Ala Ile Glu Arg Ser Val Arg Pro Leu Pro Pro His His Ala Pro
130 135 140

Ala Ala Val Pro Pro Tyr Phe Gly Ala Thr Asn Asp Asp Gly Phe Phe
145 150 155 160

Leu Pro Gly Ser Ala Asp Met Asp Ser Leu Ser Ala Ala Leu Gly Pro
165 170 175

Pro Ala Gly Arg Pro Gly Ile Leu Ser Pro Ala Ala Leu Pro Pro Ala
180 185 190

Ala Ser Thr Gly Leu Phe Ser Pro Met Pro Phe Asp Pro Ser Cys Leu
195 200 205

Ser Trp Leu Ser Glu Leu Ser Pro Phe Leu Pro Ser Ala Gly Thr Arg
210 215 220

Ala Ala Ala Ala Gly Leu Leu Asp Gln Ala Pro Phe Ala Pro Ser Pro
225 230 235 240

Arg Ser Ser Leu Leu Leu Ser Thr Pro Thr Met Pro Ser Pro Ala Thr
245 250 255

Phe Ser Val Leu Glu Phe Phe Ser Ser Pro Asn Phe Pro Asp Leu
260 265 270